SEQUENCE LISTING der Horn, Peter B. Wang, Yan MJ Bioworks, Incorporated <120> Novel Compositions With Polymerase Activity <130> 020130-001510US <140> US 10/627,582 <141> 2003-07-25 <150> US 60/398,687 <151> 2002-07-25 <150> US 60/483,287 <151> 2003-06-27 <160> 49 <170> PatentIn Ver. 2.1 <210> 1 <211> 2325 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence:full-length assembled hybrid polymerase clone Phy1

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| Tyr | Thr | Leu 275 | Glu | Ala | Val | Tyr | Glu 280 | Ala | Ile | Phe | Gly | Lys 285 | Pro | Lys | Glu |
| Lys | Val 290 | Tyr | Ala | Asp | Glu | Ile 295 | Ala | Lys | Ala | Trp | Glu 300 | Thr | Gly | Glu | Gly |
| Leu 305 | Glu | Arg | Val | Ala | Lys 310 | Tyr | Ser | Met | Glu | Asp 315 | Ala | Lys | Ala | Thr | Tyr 320 |
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| Leu 145 | Tyr | His | Glu | Gly | Glu 150 | Glu | Phe | Gly | Lys | Gly 155 | Pro | Ile | Ile | Met | Ile 160 |
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| Ser | Tyr | Ala | Asp | Glu 165 | Asn | Glu | Ala | Lys | Val 170 | Ile | Thr | Trp | Lys | Lys 175 | Ile |
| Asp | Leu | Pro | Tyr 180 | Val | Glu | Val | Val | Ser 185 | Ser | Glu | Arg | Glu | Met 190 | Ile | Lys |
| Arg | Phe | Leu 195 | Lys | Val | Ile | Arg | Glu 200 | Lys | Asp | Pro | Asp | Ile 205 | Ile | Val | Thr |
| Tyr | Asn 210 | Gly | Asp | Ser | Phe | Asp 215 | Phe | Pro | Tyr | Leu | Ala 220 | Lys | Arg | Ala | Glu |
| Lys 225 | Leu | Gly | Ile | Lys | Leu 230 | Pro | Ile | Gly | Arg | Asp 235 | Gly | Ser | Glu | Pro | Lys 240 |
| Met | Gln | Arg | Ile | Gly 245 | Asp | Met | Thr | Ala | Val 250 | Glu | Val | Lys | Gly | Arg 255 | Ile |
| His | Phe | Asp | Leu 260 | Tyr | His | Val | Ile | Arg 265 | Arg | Thr | Ile | Asn | Leu 270 | Pro | Thr |
| Tyr | Thr | Leu 275 | Glu | Ala | Val | Tyr | Glu 280 | Ala | Ile | Phe | Gly | Lys 285 | Pro | Lys | Glu |
| Lys | Val 290 | Tyr | Ala | His | Glu | Ile 295 | Ala | Glu | Ala | Trp | Glu 300 | Ser | Gly | Glu | Gly |
| | | | | | | | | | | | | | | | |
| Leu 305 | Glu | Arg | Val | Ala | Lys 310 | Tyr | Ser | Met | Glu | Asp 315 | Ala | Lys | Ala | Thr | Tyr 320 |
| 305 | | | | | 310 | _ | | | | 315 | | Lys Leu | | | 320 |
| 305 Glu | Leu | Gly | Lys | Glu 325 | 310 Phe | Phe | Pro | Met | Glu 330 | 315 Ile | Gln | _ | Ser | Arg 335 | 320 Leu |
| 305 Glu Val | Leu Gly | Gly | Lys Pro 340 | Glu 325 Leu | 310 Phe Trp | Phe Asp | Pro Val | Met Ser 345 | Glu 330 Arg | 315 Ile Ser | Gln Ser | Leu | Ser Gly 350 | Arg 335 Asn | 320 Leu Leu |
| 305 Glu Val | Leu Gly Glu | Gly Gln Trp 355 | Lys Pro 340 Phe | Glu 325 Leu Leu | 310 Phe Trp Leu | Phe Asp Arg | Pro Val Lys 360 | Met Ser 345 Ala | Glu 330 Arg Tyr | 315 Ile Ser Glu | Gln Ser Arg | Leu Thr Asn 365 | Ser Gly 350 Glu | Arg 335 Asn Leu | 320 Leu Leu |
| 305 Glu Val Val | Leu Gly Glu Asn 370 | Gly Gln Trp 355 Lys | Lys Pro 340 Phe | Glu 325 Leu Leu Ser | 310 Phe Trp Leu Glu | Phe Asp Arg Arg 375 | Pro Val Lys 360 Glu | Met Ser 345 Ala Tyr | Glu 330 Arg Tyr | 315 Ile Ser Glu Arg | Gln Ser Arg Arg 380 | Leu Thr Asn 365 | Ser Gly 350 Glu Arg | Arg 335 Asn Leu Glu | 320 Leu Leu Ala Ser |
| 305 Glu Val Val Pro | Leu Gly Glu Asn 370 | Gly Gln Trp 355 Lys Gly | Pro 340 Phe Pro | Glu 325 Leu Leu Ser | 310 Phe Trp Leu Glu Val 390 | Phe Asp Arg Arg 375 Lys | Pro Val Lys 360 Glu | Met Ser 345 Ala Tyr Pro | Glu 330 Arg Tyr Glu | 315 Ile Ser Glu Arg Lys 395 | Gln Ser Arg Arg 380 Gly | Leu Thr Asn 365 Leu | Ser Gly 350 Glu Arg | Arg 335 Asn Leu Glu | 320 Leu Leu Ala Ser Asn 400 |
| 305 Glu Val Val Pro Tyr 385 Ile | Leu Gly Glu Asn 370 Thr | Gly Gln Trp 355 Lys Gly Tyr | Pro 340 Phe Pro Gly Leu | Glu 325 Leu Leu Ser Tyr Asp 405 | 310 Phe Trp Leu Glu Val 390 Phe | Phe Asp Arg Arg 375 Lys | Pro Val Lys 360 Glu Glu Ser | Met Ser 345 Ala Tyr Pro Leu | Glu 330 Arg Tyr Glu Glu Tyr 410 | 315 Ile Ser Glu Arg Lys 395 Pro | Gln Ser Arg Arg 380 Gly Ser | Leu Thr Asn 365 Leu | Ser Gly 350 Glu Arg Trp | Arg 335 Asn Leu Glu Glu Ile 415 | January Leu Leu Ala Ser Asn 400 Thr |
| 305 Glu Val Val Pro Tyr 385 Ile | Leu Gly Glu Asn 370 Thr | Gly Gln Trp 355 Lys Gly Tyr | Pro 340 Phe Pro Gly Leu Ser 420 | Glu 325 Leu Leu Ser Tyr Asp 405 Pro | 310 Phe Trp Leu Glu Val 390 Phe Asp | Phe Asp Arg Arg 375 Lys Arg | Pro Val Lys 360 Glu Glu Ser Leu | Met Ser 345 Ala Tyr Pro Leu Asn 425 | Glu 330 Arg Tyr Glu Glu Tyr 410 Leu | 315 Ile Ser Glu Arg Lys 395 Pro | Gln Ser Arg Arg 380 Gly Ser | Leu Thr Asn 365 Leu Leu Leu Cys | Ser Gly 350 Glu Arg Trp Ile Lys 430 | Arg 335 Asn Leu Glu Glu Ile 415 Glu | January Leu Leu Ala Ser Asn 400 Thr |

| Lys 465 | Arg | Lys | Met | Lys | Ala 470 | Ser | Lys | Asp | Pro | Ile 475 | Glu | Lys | Ile | Leu | Leu 480 |
|--------------------------|--------------------------|---------------------------------|--------------------------|---------------------------------|--------------------------|---------------------------------|--------------------------|---------------------------------|--|--|---------------------------------|---------------------------------|--------------------------|--------------------------|---------------------------------|
| Asp | Tyr | Arg | Gln | Arg 485 | Ala | Ile | Lys | Leu | Leu 490 | Ala | Asn | Ser | Phe | Tyr 495 | Gly |
| Tyr | Tyr | Gly | Tyr 500 | Ala | Lys | Ala | Arg | Trp 505 | Tyr | Cys | Lys | Glu | Cys 510 | Ala | Glu |
| Ser | Val | Thr 515 | Ala | Trp | Gly | Arg | Glu 520 | Tyr | Ile | Glu | Leu | Val 525 | Arg | Lys | Glu |
| Leu | Glu 530 | Glu | Lys | Phe | Gly | Phe 535 | Lys | Val | Leu | Tyr | Ile 540 | Asp | Thr | Asp | Gly |
| Leu 545 | Tyr | Ala | Thr | Ile | Pro 550 | Gly | Gly | Lys | Ser | Glu 555 | Glu | Ile | Lys | Lys | Lys 560 |
| Ala | Leu | Glu | Phe | Val 565 | Asp | Tyr | Ile | Asn | Ser 570 | Lys | Leu | Pro | Gly | Leu 575 | Leu |
| Glu | Leu | Glu | Tyr 580 | Glu | Gly | Phe | Tyr | Lys 585 | Arg | Gly | Phe | Phe | Val 590 | Thr | Lys |
| Lys | Arg | Tyr 595 | Ala | Leu | Ile | Asp | Glu 600 | Glu | Gly | Lys | Ile | Ile 605 | Thr | Arg | Gly |
| Leu | Glu 610 | Ile | Val | Arg | Arg | Asp 615 | Trp | Ser | Glu | Ile | Ala 620 | Lys | Glu | Thr | Gln |
| Ala 625 | Lys | Val | Leu | Glu | Thr 630 | Ile | Leu | Lys | His | Gly 635 | Asn | Val | Glu | Glu | Ala 640 |
| Val | Arg | Ile | Val | Lys 645 | Glu | Val | Thr | Gln | Lys 650 | Leu | Ala | Lys | Tyr | Glu 655 | Ile |
| Pro | Pro | Glu | Lys 660 | Leu | Ala | Ile | Tyr | Glu | Gln | Ile | Thr | Pro | Pro | Leu | His |
| Glu | | | | | | | | 665 | | | 1111 | | 670 | | |
| | Tyr | Lys 675 | Ala | Ile | Gly | Pro | His 680 | 665 | | | | | | Leu | Ala |
| Ala | | 675 | | | | | 680 | 665 Val | Ala | Val | Ala | Lys 685 | Arg | Leu Ile | |
| | Arg 690 | 675 Gly | Val | Lys | Ile | Lys 695 | 680 Pro | 665 Val Gly | Ala Met | Val Val | Ala Ile 700 | Lys 685 Gly | Arg Tyr | | Val |
| Leu 705 | Arg 690 Arg | 675 Gly Gly | Val Asp | Lys Gly | Ile Pro 710 | Lys 695 Ile | 680 Pro Ser | 665 Val Gly Asn | Ala Met Arg | Val Val Ala 715 | Ala Ile 700 Ile | Lys 685 Gly Leu | Arg Tyr Ala | Ile | Val Glu 720 |
| Leu 705 Tyr | Arg 690 Arg | 675 Gly Gly Leu | Val Asp Lys | Lys Gly Lys 725 | Ile Pro 710 His | Lys 695 Ile Lys | 680 Pro Ser Tyr | 665 Val Gly Asn Asp | Ala Met Arg Ala 730 | Val Val Ala 715 Glu | Ala Ile 700 Ile Tyr | Lys 685 Gly Leu Tyr | Arg Tyr Ala Ile | Ile Glu Glu | Val Glu 720 Asn |
| Leu 705 Tyr Gln | Arg 690 Arg Asp | 675 Gly Gly Leu Leu | Val Asp Lys Pro | Lys Gly Lys 725 Ala | Ile Pro 710 His | Lys 695 Ile Lys Leu | 680 Pro Ser Tyr | Gly Asn Asp | Ala Met Arg Ala 730 Leu | Val Val Ala 715 Glu Glu | Ala Ile 700 Ile Tyr | Lys 685 Gly Leu Tyr | Tyr Ala Ile Gly 750 | Ile Glu Glu 735 | Val Glu 720 Asn Arg |

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile 785 795 Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu 810 Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys 840 <210> 7 <211> 2535 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: hybrid polymerase Sso7d fusion protein PhS5 <400> 7 atgatectgg atgetgaeta cateactgaa gaeggeaaac egattateeg tetgtteaaa 60 aaagagaacg gcgaatttaa ggttgagtat gatcgcaact ttcgtccata catttacgct 120 ctgctgagag atgattctca gattgatgaa gttaaaaaaa tcactgctga gcgccatggc 180 aagattgttc gtatcattga tgcggaaaag gtagaaaaga aatttctggg cagaccaatc 240 acceptgtgga gactgtattt cgaacatcca caagatgttc cggctattcg cgataaagtt 300 cqcqaacatc ctgcagttgt tgacatcttc gaatacgata ttccatttgc aaagcgttac 360 ctcatcgaca aaggcctgat accaatggag ggcgaggaag aactcaagct cctggcgttc 420 gatatagaaa ccctctatca cgaaggcgaa gagtttggta aaggcccaat tataatgatc 480 agctatgcag atgaaaacga agcaaaggtg attacttgga aaaaaataga tctcccatac 540 qttqaqqttq tatcttccga gcgcgagatg attaaacgtt ttctcagagt tatccgcgag 600 aaggatccgg acattatcat tacttataac ggcgactctt ttgacttccc atatctggcg 660 aaacqcqcaq aaaaactcqq tattaaactg cctctcggcc gtgatggttc cgagccgaag 720 atgcagcgta tcggcgatat gaccgctgta gaaattaagg gtcgtatcca tttcgacctg 780 tatcatgtaa ttactcgtac tattaacctc ccgacttaca ctctcgaggc tgtatatgaa 840 gcaatttttg gtaagccgaa ggagaaggta tacgccgatg agattgcaga ggcgtgggaa 900 tccggtaaga acctcgagcg tgttgcaaaa tactccatgg aagatgcaaa ggcgacttat 960 gaactcggca aagaattcct cccaatggaa atccagctct ctcgcctggt tggccaacca 1020 ctgtgggatg tttctcgttc ttccaccggt aacctcgtag agtggtatct cctgcgcaaa 1080 gcgtacgaac gcaacgaagt ggctccgaac aagccagacg aagaagagta tgaacgccgt 1140 ctccgcgagt cttacactgg tggctatgtt aaagagccag aaaagggcct ctgggaaaac 1200 ctcgtgtccc tcgattttcg cgctctgtat ccgtctatta tcattaccca caacgtgtct 1260 ccggatactc tcaaccgcga gggctgcaaa gagtatgata ttgctccgca agtaggccac 1320 aagttetgea aggaetteee gggetttatt cegtetetee tgaaacatet getegatgaa 1380 cgccaagaga ttaagcgtaa aatgaaggcg tccaaggatc cgattgaaaa aaaaatgctc 1440 gactatcgcc aaagagcgat taaactcctc gcaaactctt tttacggcta ttatggctat 1500 qcaaaaqcac qctqqtactq taaggagtgt gctgagtccg ttactgcttg gggtcgcgaa 1560 tacatcgagc tcgtgtggaa ggagctcgaa gaaaagtttg gctttaaagt tctctacatt 1620 gacactgatg gtctctatgc gactattccg ggtggtaagc ctgaggaaat taagaaaaag 1680 gctctagaat ttgtgaaata cattaactcg aagctcccgg gtctcctgga gctcgaatat 1740 gaaggetttt atgttegegg ettettegtt accaagaaga gatatgeggt gattgatgaa 1800 gaaggcaaaa ttattactcg tggtctcgag attgtgcgcc gtgattggag cgaaattgcg 1860 aaagaaactc aagctagagt tctcgaggct attctcaaac acggcaacgt tgaagaagct 1920 gtgaaaattg taaaagaagt aacccaaaag ctcgctaaat atgaaattcc gccagagaag 1980 ctcgcgattt atgagcagat tactcgcccg ctgcatgagt ataaggcgat tggtccgcac 2040 gtggctgttg caaagagact ggctgctaga ggcgtgaaag ttagaccggg tatggtaatt 2100 ggctacattg tactccgcgg cgatggtccg attagcaacc gtgcaattct agctgaggaa 2160 tacgatctga aaaagcacaa gtatgacgca gaatattaca ttgagaacca ggtgctcccg 2220

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<212> PRT

<213> Artificial Sequence

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Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile 35 40 45

Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
50 60

Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65 70 75 80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile 85 90 95

Arg Asp Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125

Met Glu Gly Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr 130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile 145 150 155 160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile 165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 180 185 190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr 195 200 205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu 210 215 220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys 225 230 235 240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile 250 His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr 265 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu Lys Val Tyr Ala Asp Glu Ile Ala Glu Ala Trp Glu Ser Gly Lys Asn 295 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu 325 330 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala 360 Pro Asn Lys Pro Asp Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr 405 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu Tyr Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly 435 Phe Ile Pro Ser Leu Leu Lys His Leu Leu Asp Glu Arg Gln Glu Ile Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Lys Met Leu 465 Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu 500 505 510 Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Leu Val Trp Lys Glu 520 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly 535 540 Leu Tyr Ala Thr Ile Pro Gly Gly Lys Pro Glu Glu Ile Lys Lys 550 555 560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu 565 570 Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys 585 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala Arg Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala Val Lys Ile Val Lys Glu Val Thr Gln Lys Leu Ala Lys Tyr Glu Ile 650 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala 680 Ala Arg Gly Val Lys Val Arg Pro Gly Met Val Ile Gly Tyr Ile Val 695 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu 715 Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Val Gly Leu Thr Ser Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Ala Thr Val Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile 785 Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu 810 Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro 825 830 Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys

840

835

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<212> DNA

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<223> Description of Artificial Sequence:hybrid polymerase Sso7d fusion protein PhS7

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cgcgaacatc ctgcagttgt tgacatcttc gaatacgata ttccatttgc aaagcgttac 360
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<210> 10
<211> 844
<212> PRT
<213> Artificial Sequence
<220>
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<223> Description of Artificial Sequence:hybrid
 polymerase Sso7d fusion protein PhS7

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 20 25 30
- Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile 35 40 45
- Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
 50 60
- Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile 65 70 75 80
- Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
 85 90 95
- Arg Asp Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
 100 105 110
- Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125
- Met Glu Gly Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr 130 135 140
- Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile 145 150 155 160
- Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile 165 170 175
- Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 180 185 190
- Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ihr 195 200 205
- Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu 210 215 220
- Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys 225 230 235 240
- Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile 245 250 255
- His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
 260 265 270
- Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu 275 280 285
- Lys Val Tyr Ala Asp Glu Ile Ala Glu Ala Trp Glu Ser Gly Lys Asn 290 295 300
- Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr 305 310 315 320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu 325 330 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala Pro Asn Lys Pro Asp Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr 410 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Asn Tyr Asp Val Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly 440 Phe Ile Pro Ser Leu Leu Gly Arg Leu Leu Glu Glu Arg Gln Glu Ile Lys Thr Lys Met Lys Ala Thr Lys Asp Pro Ile Glu Lys Lys Leu Leu Asp Tyr Arg Gln Lys Ala Ile Lys Ile Leu Ala Asn Ser Phe Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Phe Val Arg Lys Glu Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly Leu Tyr Ala Thr Ile Pro Gly Gly Lys Pro Glu Glu Ile Lys Lys Lys 560 550 Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu 570 Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala Arg Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala 630

Val Lys Ile Val Lys Glu Val Thr Gln Lys Leu Ala Lys Tyr Glu Ile 645 650 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His 660 665 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala 680 Ala Arg Gly Val Lys Val Arg Pro Gly Met Val Ile Gly Tyr Ile Val 695 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn 730 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Val Gly Leu Thr Ser 760 Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Ala Thr Val Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile 795 Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys <210> 11 <211> 2337 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: hybrid polymerase Hyb1 <220> <221> modified base <222> (1416) <223> n = g, a, c or tatgateetgg atgetgaeta cateaetgaa gaeggeaaac eggttateeg tetetteaaa 60 aaagagaacg gcgaatttaa gattgagtat gatcgcacct ttcgtccata catttacgct 120 ctgctgagag atgattctaa gattgaggaa gttagaaaaa tcactgctga gcgccatggc 180 aagattgttc gtatcgttga tgtggaaaag gtaaggaaga aatttctggg cagaccaatc 240 aaggtgtgga gactgtattt cgaacatcca caagatgttc cgactattcg cgataaagtt 300

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Glu Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg

50

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| Lys | Val | Trp | Arg | Leu 85 | Tyr | Phe | Glu | His | Pro 90 | Gln | Asp | Val | Pro | Thr 95 | Ile |
| Arg | Asp | Lys | Val 100 | Arg | Glu | His | Pro | | Val | Ile | Asp | Ile | Phe 110 | Glu | Tyr |
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| Leu 145 | Tyr | His | Gly | Ser | Glu 150 | Glu | Phe | Gly | Lys | Gly 155 | Pro | Ile | Ile | Met | Ile 160 |
| Ser | Tyr | Ala | Asp | Glu 165 | Asn | Glu | Ala | Lys | Val 170 | Ile | Thr | Trp | Lys | Asn 175 | Ile |
| Asp | Leu | Pro | Tyr 180 | Val | Glu | Val | Val | Ser 185 | Ser | Glu | Arg | Glu | Met 190 | Ile | Lys |
| Arg | Phe | Leu 195 | Arg | Ile | Ile | Arg | Glu 200 | Lys | Asp | Pro | Asp | Ile 205 | Ile | Val | Thr |
| Tyr | Asn 210 | Gly | Asp | Ser | Phe | Asp 215 | Leu | Pro | Tyr | Leu | Ala 220 | Lys | Arg | Ala | Glu |
| | _ | ~ 7 | ~ 7 | T | _ | _, | . | 01 | 7 | 7 | a 1 | Crra | a 1 | 77- | T |
| Lys 225 | Leu | GIY | lle | гуѕ | Leu 230 | Thr | Leu | GIY | arg | 235 | GIY | Cys | GIU | АІа | Lys 240 |
| 225 | | | | _ | 230 | | | | | 235 | | | | Arg 255 | 240 |
| 225 Met | Gln | Arg | Leu | Gly 245 | 230 Asp | Met | Thr | Ala | Val 250 | 235 Glu | Val | Lys | Gly | Arg | 240 Ile |
| 225 Met His | Gln Phe | Arg Asp | Leu Leu 260 | Gly 245 Tyr | 230 Asp Tyr | Met Val | Thr Ile | Ala Ser 265 | Val 250 Arg | 235 Glu Thr | Val Ile | Lys Asn | Gly Leu 270 | Arg 255 | 240 Ile Thr |
| 225 Met His | Gln Phe Thr | Arg Asp Leu 275 | Leu Leu 260 Glu | Gly 245 Tyr | 230 Asp Tyr Val | Met Val Tyr | Thr Ile Glu 280 | Ala Ser 265 Ala | Val 250 Arg | 235 Glu Thr Phe | Val Ile Gly | Lys Asn Lys 285 | Gly Leu 270 Pro | Arg 255 Pro | 240 Ile Thr |
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| 225 Met His Tyr Lys Leu 305 | Gln Phe Thr Val 290 Glu | Arg Asp Leu 275 Tyr | Leu Leu 260 Glu Ala Val | Gly 245 Tyr Ala Asp | 230 Asp Tyr Val Asp Lys 310 | Met Val Tyr Ile 295 | Thr Ile Glu 280 Ala Ser | Ala Ser 265 Ala Glu Met | Val 250 Arg Ile Ala Glu | 235 Glu Thr Phe Trp Asp 315 | Val Ile Gly Glu 300 Ala | Lys Asn Lys 285 Thr | Gly Leu 270 Pro Gly Ala | Arg 255 Pro Lys | 240 Ile Thr Glu Gly Tyr 320 |
| 225 Met His Tyr Lys Leu 305 Glu | Gln Phe Thr Val 290 Glu Leu | Arg Asp Leu 275 Tyr Arg | Leu Leu 260 Glu Ala Val | Gly 245 Tyr Ala Asp Ala Glu 325 | 230 Asp Tyr Val Asp Lys 310 Phe | Met Val Tyr Ile 295 Tyr | Thr Ile Glu 280 Ala Ser | Ala Ser 265 Ala Glu Met | Val 250 Arg Ile Ala Glu Glu 330 | 235 Glu Thr Phe Trp Asp 315 Ala | Val Ile Gly Glu 300 Ala | Lys Asn Lys 285 Thr Lys | Gly Leu 270 Pro Gly Ala Ser | Arg 255 Pro Lys Lys Thr | 240 Ile Thr Glu Gly Tyr 320 Leu |
| 225 Met His Tyr Lys Leu 305 Glu Val | Gln Phe Thr Val 290 Glu Leu Gly | Arg Leu 275 Tyr Arg Gly | Leu Leu 260 Glu Ala Val Lys Pro 340 | Gly 245 Tyr Ala Asp Ala Glu 325 Leu | 230 Asp Tyr Val Asp Lys 310 Phe Trp | Met Val Tyr Ile 295 Tyr Leu Asp | Thr Ile Glu 280 Ala Ser Pro | Ala Ser 265 Ala Glu Met Met Ser 345 | Val 250 Arg Ile Ala Glu Glu 330 Arg | 235 Glu Thr Phe Trp Asp 315 Ala Ser | Val Ile Gly Glu 300 Ala Gln Ser | Lys Asn Lys 285 Thr Lys Leu Thr | Gly Leu 270 Pro Gly Ala Ser Gly 350 | Arg 255 Pro Lys Lys Thr | 240 Ile Thr Glu Gly Tyr 320 Leu Leu |

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|---|---|---------------------------------|--|--------------------------|---------------------------------|--|---|---------------------------------|---------------------------------|--------------------------|--|---|---|
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| His Asn V | Val Ser 420 | Pro | Asp | Thr | Leu | Asn 425 | Arg | Glu | Gly | Cys | Lys 430 | Asp | Tyr |
| Asp Ile A | Ala Pro 435 | Glu | Val | Gly | His 440 | Lys | Phe | Cys | Lys | Asp 445 | Phe | Leu | Gly |
| Phe Ile 1 450 | Pro Ser | Leu | Leu | Gly 455 | His | Leu | Leu | Glu | Glu 460 | Arg | Gln | Glu | Ile |
| Lys Thr 1 465 | Lys Met | Lys | Glu 470 | Thr | Xaa | Asp | Pro | Ile 475 | Glu | Lys | Ile | Leu | Leu 480 |
| Asp Tyr A | Arg Gln | Lys 485 | Ala | Ile | Lys | Leu | Leu 490 | Ala | Asn | Ser | Tyr | Tyr 495 | Gly |
| Tyr Tyr (| Gly Tyr 500 | Ala | Lys | Ala | Arg | Trp 505 | Tyr | Cys | Lys | Glu | Cys 510 | Ala | Glu |
| Ser Val : | Thr Ala 515 | Trp | Gly | Arg | Glu 520 | Tyr | Ile | Glu | Phe | Val 525 | Trp | Lys | Glu |
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| Leu Tyr A | Ala Thr | Ile | | Gly | Gly | Glu | Pro | | Glu | Ile | Lys | Lys | _ |
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| Ala Leu (Glu Leu (Lys Arg | Glu Tyr 580 Tyr Ala 595 | 565 Glu Val | Lys Gly Ile | Phe Asp | Tyr Glu 600 | Lys 585 Glu | 570 Arg Gly | Lys Gly Lys | Phe Ile | Phe Ile 605 | Val 590 Thr | 575 Thr Arg | Leu Lys Gly |
| Ala Leu (Glu Leu (Lys Arg (Leu Glu Leu Glu Leu Glu Channa | Glu Tyr 580 Tyr Ala 595 Ile Val | 565 Glu Val Arg | Lys Gly Ile Arg | Phe Asp Asp 615 | Tyr Glu 600 Trp | Lys 585 Glu Ser | 570 Arg Gly Glu | Lys Gly Lys Ile | Phe Ile Ala 620 | Phe Ile 605 Lys | Val 590 Thr | 575 Thr Arg Thr | Leu Lys Gly Gln |
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Phe Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
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                             40
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Lys Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
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                                105
                                                    110
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Met Glu Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
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35

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| Leu 145 | Tyr | His | Glu | Gly | Glu 150 | Glu | Phe | Ala | Lys | Gly 155 | Pro | Ile | Ile | Met | Ile 160 |
| Ser | Tyr | Ala | Asp | Glu 165 | Asp | Glu | Ala | Lys | Val 170 | Ile | Thr | Trp | Lys | Lys 175 | Ile |
| Asp | Leu | Pro | Tyr 180 | Val | Glu | Val | Val | Ser 185 | Ser | Glu | Arg | Glu | Met 190 | Ile | Lys |
| Arg | Phe | Leu 195 | Arg | Val | Ile | Arg | Glu 200 | Lys | Asp | Pro | Asp | Val 205 | Ile | Val | Thr |
| Tyr | Asn 210 | Gly | Asp | Ser | Phe | Asp 215 | Leu | Pro | Tyr | Leu | Ala 220 | Lys | Arg | Ala | Glu |
| Lys 225 | Leu | Gly | Ile | Lys | Leu 230 | Pro | Leu | Gly | Arg | Asp 235 | Gly | Ser | Glu | Pro | Lys 240 |
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| His | Phe | Asp | Leu 260 | Tyr | His | Val | Ile | Ser 265 | Arg | Thr | Ile | Asn | Leu 270 | Pro | Thr |
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Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly 485 490 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu 505 Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu 520 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu 570 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly 600 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala 630 Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile 645 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu 715 Phe Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn 730 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg 745 750 Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Ala Gly Leu Thr Ala Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Ala Thr Val Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile 785 790 795

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu 805 810 Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro 820 825 Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys 835 840 <210> 21 <211> 189 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: Sso7d coding region <400> 21 accgtaaagt tcaagtacaa aggcgaagaa aaagaggtag acatctccaa gatcaagaaa 60 gtatggcgtg tgggcaagat gatctccttc acctacgacg agggcggtgg caagaccggc 120 cgtggtgcgg taagcgaaaa ggacgcgcg aaggagctgc tgcagatgct ggagaagcag 180 aaaaagtga <210> 22 <211> 63 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Sso7d binding domain <400> 22 Ala Thr Val Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys 40 Asp Ala Pro Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys 60 <210> 23 <211> 25 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence:signature

invariable sequence element in hybrid polymerases

containing nucleotide binding motif

<400> 23

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1 10 15

Ala Glu Ser Val Thr Ala Trp Gly Arg
20 25

<210> 24

<211> 775

<212> PRT

<213> Pyrococcus furiosus

<220>

<223> parent Pyrococcus furiosus family B DNA polymerase PolI (Pfu)

<400> 24

Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
1 5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
20 25 30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile 35 40 45

Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
50 55 60

Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
65 70 75 80

Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile 85 90 95

Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125

Met Glu Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr 130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile 145 150 155 160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile 165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 180 185 190

Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
195 200 205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu 210 215 220

Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys 230 Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile 250 His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr 265 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu 280 Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu 345 Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser 375 Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ihr 405 His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly 485 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu 515 520 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly 530 535 540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys 550 555 Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu 570 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys 585 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly 600 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln 615 Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His 665 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn 730 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr Ser Trp Leu Asn Ile Lys Lys Ser 770 <210> 25 <211> 775 <212> PRT <213> Pyrococcus sp. <220> <223> parent Pyrococcus sp. strain GD-B PolI (Deep Vent) DNA polymerase

41

30

Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg

25

<400> 25

20

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Gln Ile 40 Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg Ile Ile Asp Ala Glu Lys Val Arg Lys Lys Phe Leu Gly Arg Pro Ile Glu Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile Arg Asp Lys Ile Arg Glu His Ser Ala Val Ile Asp Ile Phe Glu Tyr Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro Met Glu Gly Asp Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr Leu Tyr His Glu Gly Glu Phe Ala Lys Gly Pro Ile Ile Met Ile Ser Tyr Ala Asp Glu Glu Glu Ala Lys Val Ile Thr Trp Lys Lys Ile Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 185 Arg Phe Leu Lys Val Ile Arg Glu Lys Asp Pro Asp Val Ile Ile Thr Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Val Lys Arg Ala Glu 215 Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu Lys Val Tyr Ala His Glu Ile Ala Glu Ala Trp Glu Thr Gly Lys Gly 295 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu 325 330 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu 340 345

Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala 360 Pro Asn Lys Pro Asp Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser Tyr Ala Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Gly 390 395 Leu Val Ser Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr 405 410 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Glu Tyr 425 Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe Ile Pro Ser Leu Leu Lys Arg Leu Leu Asp Glu Arg Gln Glu Ile Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Lys Met Leu 475 Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Arg Lys Glu 515 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly 535 Leu Tyr Ala Thr Ile Pro Gly Ala Lys Pro Glu Glu Ile Lys Lys Ala Leu Glu Phe Val Asp Tyr Ile Asn Ala Lys Leu Pro Gly Leu Leu Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys Lys Lys Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln 615 Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala Val Lys Ile Val Lys Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Ile 645 650 Pro Pro Glu Lys Leu Val Ile Tyr Glu Gln Ile Thr Arg Pro Leu His 660 665 670

- Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala 675 680 685
- Ala Arg Gly Val Lys Val Arg Pro Gly Met Val Ile Gly Tyr Ile Val 690 695 700
- Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu 705 710 715 720
- Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn 725 730 735
- Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
 740 745 750
- Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Thr Gly Leu Thr Ala 755 760 765
- Trp Leu Asn Ile Lys Lys Lys 770 775
- <210> 26
- <211> 775
- <212> PRT
- <213> Artificial Sequence
- <220>
- <223> Description of Artificial Sequence:designed hybrid polymerase
- <220>
- <221> MOD RES
- <222> (1)..(775)
- <223> Xaa = unknown amino acid
- <400> 26
- Met Ile Leu Asp Xaa Asp Tyr Ile Thr Glu Xaa Gly Lys Pro Xaa Ile 1 5 10 15
- Arg Xaa Phe Lys Lys Glu Asn Gly Xaa Phe Lys Xaa Glu Xaa Asp Arg
 20 25 30
- Xaa Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Xaa Asp Asp Ser Xaa Ile 35 40 45
- Xaa Glu Val Xaa Lys Ile Thr Xaa Glu Arg His Gly Lys Ile Val Arg 50 55 60
- Ile Xaa Asp Xaa Glu Lys Val Xaa Lys Lys Phe Leu Gly Xaa Pro Ile 65 70 75 80
- Xaa Val Trp Xaa Leu Tyr Xaa Glu His Pro Gln Asp Val Pro Xaa Ile 85 90 95
- Arg Xaa Lys Xaa Arg Glu His Xaa Ala Val Xaa Asp Ile Phe Glu Tyr 100 105 110
- Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125

Met Glu Gly Xaa Glu Glu Leu Lys Xaa Leu Ala Phe Asp Ile Glu Thr 135 Leu Tyr His Glu Gly Glu Phe Xaa Lys Gly Pro Ile Ile Met Ile 150 155 Ser Tyr Ala Asp Glu Xaa Glu Ala Lys Val Ile Thr Trp Lys Xaa Ile 170 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys Arg Phe Leu Xaa Xaa Ile Arg Glu Lys Asp Pro Asp Xaa Ile Xaa Thr Tyr Asn Gly Asp Ser Phe Asp Xaa Pro Tyr Leu Xaa Lys Arg Ala Glu Lys Leu Gly Ile Lys Leu Xaa Xaa Gly Arg Asp Gly Ser Glu Pro Lys Met Gln Arg Xaa Gly Asp Met Thr Ala Val Glu Xaa Lys Gly Arg Ile 250 His Phe Asp Leu Tyr His Val Ile Xaa Arg Thr Ile Asn Leu Pro Thr Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu 280 Lys Val Tyr Ala Xaa Glu Ile Ala Xaa Ala Trp Glu Xaa Gly Xaa Xaa Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Xaa Thr Tyr Glu Leu Gly Xaa Glu Phe Xaa Pro Met Glu Xaa Gln Leu Ser Arg Leu Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu Val Glu Trp Xaa Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Xaa Ala 355 Pro Asn Lys Pro Xaa Glu Xaa Glu Tyr Xaa Arg Arg Leu Arg Glu Ser Tyr Xaa Gly Gly Xaa Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Xaa 385 395 Xaa Val Xaa Leu Asp Phe Arg Xaa Leu Tyr Pro Ser Ile Ile Ile Thr 405 His Asn Val Ser Pro Asp Thr Leu Asn Xaa Glu Gly Cys Xaa Xaa Tyr Asp Xaa Ala Pro Xaa Val Gly His Lys Phe Cys Lys Asp Xaa Pro Gly 435 440

Phe Ile Pro Ser Leu Leu Xaa Xaa Leu Leu Xaa Glu Arg Gln Xaa Ile 455 Lys Xaa Lys Met Lys Xaa Xaa Xaa Asp Pro Ile Glu Lys Xaa Xaa Leu 470 475 Asp Tyr Arg Gln Xaa Ala Ile Lys Xaa Leu Ala Asn Ser Xaa Tyr Gly 485 490 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu 505 Ser Val Thr Ala Trp Gly Arg Xaa Tyr Ile Glu Xaa Val Xaa Lys Glu 520 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly Leu Tyr Ala Thr Ile Pro Gly Xaa Xaa Kaa Glu Glu Ile Lys Lys Ala Leu Glu Phe Val Lys Tyr Ile Asn Xaa Lys Leu Pro Gly Leu Leu 570 Glu Leu Glu Tyr Glu Gly Phe Tyr Xaa Arg Gly Phe Phe Val Thr Lys Lys Xaa Tyr Ala Xaa Ile Asp Glu Glu Gly Lys Xaa Ile Thr Arg Gly 600 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala Xaa Val Leu Glu Xaa Ile Leu Lys His Gly Xaa Val Glu Glu Ala 630 Val Xaa Ile Val Lys Glu Val Xaa Xaa Lys Leu Xaa Xaa Tyr Glu Ile 645 Pro Pro Glu Lys Leu Xaa Ile Tyr Glu Gln Ile Thr Arg Pro Leu His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Xaa Leu Ala Ala Xaa Gly Val Lys Xaa Xaa Pro Gly Met Val Ile Gly Tyr Ile Val Leu Arg Gly Asp Gly Pro Ile Ser Xaa Arg Ala Ile Leu Ala Glu Glu 715 Xaa Asp Xaa Xaa Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Xaa Phe Gly Tyr Arg 745 750

Lys Glu Asp Leu Arg Xaa Gln Lys Thr Xaa Gln Xaa Gly Leu Thr Xaa 755 760 765

Trp Leu Asn Ile Lys Lys Ser 770 775

<210> 27

<211> 783

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:designed hybrid
polymerase from Figure 1

<220>

<221> MOD RES

<222> (1)..(783)

<223> Xaa = unknown amino acid

<400> 27

Met Ile Leu Asp Xaa Asp Tyr Ile Thr Glu Xaa Gly Lys Pro Xaa Ile 1 5 10 15

Arg Xaa Phe Lys Lys Glu Asn Gly Xaa Phe Lys Xaa Glu Xaa Asp Arg 20 25 30

Xaa Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Xaa Asp Asp Ser Xaa Ile 35 40 45

Xaa Glu Val Xaa Lys Ile Thr Xaa Glu Arg His Gly Lys Ile Val Arg
50 55 60

Ile Xaa Asp Xaa Glu Lys Val Xaa Lys Lys Phe Leu Gly Xaa Pro Ile 65 70 75 80

Xaa Val Trp Xaa Leu Tyr Xaa Glu His Pro Gln Asp Val Pro Xaa Ile 85 90 95

Arg Xaa Lys Xaa Arg Glu His Xaa Ala Val Xaa Asp Ile Phe Glu Tyr 100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125

Met Glu Gly Xaa Glu Glu Leu Lys Xaa Leu Ala Phe Asp Ile Glu Thr 130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Xaa Lys Gly Pro Ile Ile Met Ile 145 150 155 160

Ser Tyr Ala Asp Glu Xaa Glu Ala Lys Val Ile Thr Trp Lys Xaa Ile 165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys

Arg Phe Leu Xaa Xaa Ile Arg Glu Lys Asp Pro Asp Xaa Ile Xaa Thr 195 200 205

Tyr Asn Gly Asp Ser Phe Asp Xaa Pro Tyr Leu Xaa Lys Arg Ala Glu 215 Lys Leu Gly Ile Lys Leu Xaa Xaa Gly Arg Asp Gly Ser Glu Pro Lys 230 235 Met Gln Arg Xaa Gly Asp Met Thr Ala Val Glu Xaa Lys Gly Arg Ile 250 His Phe Asp Leu Tyr His Val Ile Xaa Arg Thr Ile Asn Leu Pro Thr 265 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu 280 Lys Val Tyr Ala Xaa Glu Ile Ala Xaa Ala Trp Glu Xaa Gly Xaa Xaa 295 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Xaa Thr Tyr Glu Leu Gly Xaa Glu Phe Xaa Pro Met Glu Xaa Gln Leu Ser Arg Leu 330 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu Val Glu Trp Xaa Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Xaa Ala 360 Pro Asn Lys Pro Xaa Glu Xaa Glu Tyr Xaa Arg Arg Leu Arg Glu Ser 375 Tyr Xaa Gly Gly Xaa Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Xaa 390 Xaa Val Xaa Leu Asp Phe Arg Xaa Leu Tyr Pro Ser Ile Ile Ihr 405 His Asn Val Ser Pro Asp Thr Leu Asn Xaa Glu Gly Cys Xaa Xaa Tyr Asp Xaa Ala Pro Xaa Val Gly His Lys Phe Cys Lys Asp Xaa Pro Gly Phe Ile Pro Ser Leu Leu Xaa Xaa Leu Leu Xaa Glu Arg Gln Xaa Ile Lys Xaa Lys Met Lys Xaa Xaa Xaa Asp Pro Ile Glu Lys Xaa Xaa Leu 470 475 Asp Tyr Arg Gln Xaa Ala Ile Lys Xaa Leu Ala Asn Ser Xaa Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu 500 505 510 Ser Val Thr Ala Trp Gly Arg Xaa Tyr Ile Glu Xaa Val Xaa Lys Glu 515 520

- Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly 530 535 540
- Leu Tyr Ala Thr Il'e Pro Gly Xaa Xaa Xaa Glu Glu Ile Lys Lys 545 550 560
- Ala Leu Glu Phe Val Lys Tyr Ile Asn Xaa Lys Leu Pro Gly Leu Leu 565 570 575
- Glu Leu Glu Tyr Glu Gly Phe Tyr Xaa Arg Gly Phe Phe Val Thr Lys
 580 585 590
- Lys Xaa Tyr Ala Xaa Ile Asp Glu Glu Gly Lys Xaa Ile Thr Arg Gly 595 600 605
- Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln 610 615 620
- Ala Xaa Val Leu Glu Xaa Ile Leu Lys His Gly Xaa Val Glu Glu Ala 625 630 635 640
- Val Xaa Ile Val Lys Glu Val Xaa Xaa Lys Leu Xaa Xaa Tyr Glu Ile 645 650 655
- Pro Pro Glu Lys Leu Xaa Ile Tyr Glu Gln Ile Thr Arg Pro Leu His 660 665 670
- Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Xaa Leu Ala 675 680 685
- Ala Xaa Gly Val Lys Xaa Xaa Pro Gly Met Val Ile Gly Tyr Ile Val 690 695 700
- Leu Arg Gly Asp Gly Pro Ile Ser Xaa Arg Ala Ile Leu Ala Glu Glu 705 710 715 720
- Xaa Asp Xaa Xaa Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn 725 730 735
- Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Xaa Phe Gly Tyr Arg 740 745 750
- Lys Glu Asp Leu Arg Xaa Gln Lys Thr Xaa Gln Xaa Gly Leu Thr Xaa 755 760 765
- Trp Leu Asn Ile Lys Lys Ser Gly Thr His Asn Cys Asn His Asp 770 775 780
- <210> 28
- <211> 845
- <212> PRT
- <213> Artificial Sequence
- <220>
- <223> Description of Artificial Sequence:hybrid polymerase HyS1 from Figure 5

- <220>
- <221> MOD RES
- <222> (472)
- <223> Xaa = unknown amino acid
- <400> 28
- Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile 1 5 10 15
- Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Glu Tyr Asp Arg
 20 25 30
- Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile 35 40 45
- Glu Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
 50 60
- Ile Val Asp Val Glu Lys Val Arg Lys Lys Phe Leu Gly Arg Pro Ile 65 70 75 80
- Lys Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile 85 90 95
- Arg Asp Lys Val Arg Glu His Pro Ala Val Ile Asp Ile Phe Glu Tyr
 100 105 110
- Asp Ile Ala Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125
- Met Glu Gly Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr 130 135 140
- Leu Tyr His Gly Ser Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile 145 150 155 160
- Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile 165 170 175
- Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 180 185 190
- Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr 195 200 205
- Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu 210 215 220
- Lys Leu Gly Ile Lys Leu Thr Leu Gly Arg Asp Gly Cys Glu Ala Lys 225 230 235 240
- Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile 245 250 255
- His Phe Asp Leu Tyr Tyr Val Ile Ser Arg Thr Ile Asn Leu Pro Thr 260 265 270
- Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu 275 280 285

Lys Val Tyr Ala Asp Asp Ile Ala Glu Ala Trp Glu Thr Gly Lys Gly 295 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr 310 315 Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ala Gln Leu Ser Arg Leu 325 330 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu 345 Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala Pro Asn Lys Pro Tyr Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser 375 Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Ser Leu Val Ser Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ihr 410 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly 440 Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile . 455 Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys 545 560 Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu 565 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys 585 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly 595 600 605

```
Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln 610 615 620
```

- Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala 625 630 635 640
- Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile 645 650 655
- Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670
- Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala 675 680 685
- Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val 690 695 700
- Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu 705 710 715 720
- Phe Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn 725 730 735
- Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg 740 745 750
- Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Ala Gly Leu Thr Ala
 755 760 765
- Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
 770 780
- Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile 785 790 795 800
- Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu 805 810 815
- Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro 820 825 830
- Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn 835 840 845

<220>

<223> Description of Artificial Sequence:hybrid
 polymerase Hyb2 from Figure 5

<220>

<221> MOD RES

<222> (472)

<223> Xaa = unknown amino acid

<210> 29

<211> 758

<212> PRT

<213> Artificial Sequence

<400> 29 Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro Met Glu Gly Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr 135 Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile 170 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile 245 His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu 275 280 Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp

315

295

310

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr

Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu 325 330 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu 345 Val Glu Trp Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala 360 Pro Asn Lys Pro Ala Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser 375 Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asp 390 Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly 440 Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile 455 Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu 470 475 Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu 515 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys 585 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln 615 Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala 625 630 635

Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile 645 650 655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
660 665 670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala 675 680 685

Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val 690 695 700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu 705 710 715 720

Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn 725 730 735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
740 745 750

Lys Glu Asp Leu Arg Asn 755

<210> 30

<211> 758

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid polymerase Hyb3 from Figure 5

<220>

<221> MOD_RES

<222> (472)

<223> Xaa = unknown amino acid

<400> 30

Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile 1 5 10 15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
20 25 30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile 35 40 45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
50 60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65 70 75 80

Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile 85 90 95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr 100 105 110

| Asp | Ile | Pro 115 | Phe | Ala | Lys | Ser | Tyr 120 | Leu | Ile | Asp | Lys | Gly 125 | Leu | Ile | Pro |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met | Glu 130 | Gly | Glu | Glu | Glu | Leu 135 | Lys | Leu | Leu | Ala | Phe 140 | Asp | Ile | Glu | Thr |
| Leu 145 | Tyr | His | Glu | Gly | Glu 150 | Glu | Phe | Ala | Lys | Gly 155 | Pro | Ile | Ile | Met | Ile 160 |
| Ser | Tyr | Ala | Asp | Glu 165 | Asp | Glu | Ala | Lys | Val 170 | Ile | Thr | Trp | Lys | Lys 175 | Ile |
| Asp | Leu | Pro | Tyr 180 | Val | Glu | Val | Val | Ser 185 | Ser | Glu | Arg | Glu | Met 190 | Ile | Lys |
| Arg | Phe | Leu 195 | Arg | Val | Ile | Arg | Glu 200 | Lys | Asp | Pro | Asp | Val 205 | Ile | Val | Thr |
| Tyr | Asn 210 | Gly | Asp | Ser | Phe | Asp 215 | Leu | Pro | Tyr | Leu | Ala 220 | Lys | Arg | Ala | Glu |
| Lys 225 | Leu | Gly | Ile | Lys | Leu 230 | Pro | Leu | Gly | Arg | Asp 235 | Gly | Ser | Glu | Pro | Lys 240 |
| Met | Gln | Arg | Leu | Gly 245 | Asp | Met | Thr | Ala | Val 250 | Glu | Val | Lys | Gly | Arg 255 | Ile |
| His | Phe | Asp | Leu 260 | Tyr | His | Val | Ile | Ser 265 | Arg | Thr | Ile | Asn | Leu 270 | Pro | Thr |
| Tyr | Thr | Leu 275 | Glu | Ala | Val | Tyr | Glu 280 | Ala | Ile | Phe | Gly | Lys 285 | Pro | Lys | Glu |
| Lys | Val 290 | Tyr | Ala | Asp | Glu | Ile 295 | Ala | Gly | Ala | Trp | Glu 300 | Thr | Gly | Gĺu | Asp |
| Leu 305 | Glu | Arg | Val | Ala | Lys 310 | Tyr | Ser | Met | Glu | Asp 315 | Ala | Lys | Ala | Ile | Tyr 320 |
| Glu | Leu | Gly | Lys | Glu 325 | Phe | Phe | Pro | Met | Glu 330 | Val | Gln | Leu | Pro | Arg 335 | Leu |
| Val | Gly | Gln | Pro 340 | | Trp | Asp | Val | Ser 345 | Arg | Ser | Ser | Thr | Gly 350 | Asn | Leu |
| Val | Glu | Trp 355 | Leu | Leu | Leu | Arg | Lys 360 | Ala | Tyr | Glu | Arg | Asn 365 | Glu | Leu | Ala |
| Pro | Asn 370 | Lys | Pro | Ala | Glu | Gln 375 | Glu | Tyr | Glu | Arg | Arg 380 | Leu | Arg | Glu | Ser |
| Tyr 385 | Thr | Gly | Gly | Phe | Val 390 | Lys | Glu | Pro | Glu | Lys 395 | Gly | Leu | Trp | Glu | Asp 400 |
| Leu | Val | Ser | Leu | Asp | Phe | Arg | Ala | Leu | Tyr 410 | Pro | Ser | Ile | Ile | Ile 415 | Thr |
| | | | | | | | | | | | | | | | |

Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly 440 Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile 455 Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu 470 Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys 585 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln 615 Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val 695 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn 725 730 735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg 740 745 Lys Glu Asp Leu Arg Asn 755 <210> 31 <211> 845 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence:hybrid polymerase HyS4 from Figure 5 <220> <221> MOD_RES <222> (472) <223> Xaa = unknown amino acid <400> 31

Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
1 5 10 15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
20 25 30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile 35 40 45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
50 55 60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65 70 75 80

Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile 85 90 95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr 100 105 110

Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125

Met Glu Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr 130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile 145 150 155 160

Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile 165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 180 185 190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
195 200 205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu 215 Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys 230 Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile 250 His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu 330 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu Val Glu Trp Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala 360 Pro Asn Lys Pro Ala Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asp Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr 405 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu 470 465 475 Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu 500 505 Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu 515 520

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly 535 Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys 550 555 Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu 565 570 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys 585 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly 600 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile 650 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala 680 Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu 710 715 Phe Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn 725 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Ala Gly Leu Thr Ala Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Ala Thr Val Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu 810 Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro 820 825 830 Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn 835 840

- <210> 32
- <211> 845
- <212> PRT
- <213> Artificial Sequence
- <220>
- <223> Description of Artificial Sequence:hybrid
 polymerase PhS1 from Figure 5
- <400> 32
- Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile

 1 5 10 15
- Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Glu His Asp Arg
 20 25 30
- Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
 35 40 45
- Glu Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg 50 55 60
- Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile 65 70 75 80
- Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile 85 90 95
- Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
 100 105 110
- Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125
- Met Glu Gly Asp Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr 130 135 140
- Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile 145 150 155 160
- Ser Tyr Ala Asp Glu Glu Glu Ala Lys Val Ile Thr Trp Lys Lys Ile 165 170 175
- Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 180 185 190
- Arg Phe Leu Lys Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr 195 200 205
- Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu 210 215 220
- Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys 225 230 235 240
- Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
 245 250 255
- His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr 260 265 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu 280 Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Thr Gly Glu Gly Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu 330 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala Pro Asn Lys Pro Asp Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser Tyr Ala Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn 390 Ile Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr 405 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Asn Tyr Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe Ile Pro Ser Leu Leu Lys Arg Leu Leu Asp Glu Arg Gln Lys Ile Lys Thr Lys Met Lys Ala Ser Gln Asp Pro Ile Glu Lys Ile Met Leu Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu 505 Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly 530 535 Leu Tyr Ala Thr Ile Pro Gly Gly Lys Ser Glu Glu Ile Lys Lys Lys Ala Leu Glu Phe Val Asp Tyr Ile Asn Ala Lys Leu Pro Gly Leu Leu 565 570 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys 580 585

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Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln 610
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Ala Arg Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala 625 630 635 640

Val Arg Ile Val Lys Glu Val Thr Gln Lys Leu Ser Lys Tyr Glu Ile 645 650 655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
660 665 670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala 675 680 685

Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val 690 695 700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu 705 710 715 720

Tyr Asp Pro Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn 725 730 735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg 740 745 750

Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Thr Gly Leu Thr Ser 755 760 765

Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val 770 775 780

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile 785 790 795 800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu 805 810 815

Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro 820 825 830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn 835 840 845

<210> 33

<211> 845

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid
 polymerase PhS2 from Figure 5

<400> 33

Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile 1 5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile 40 Asp Glu Val Arg Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg Ile Ile Asp Ala Glu Lys Val Arg Lys Lys Phe Leu Gly Lys Pro Ile Glu Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro Met Glu Gly Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr 135 Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile 170 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys .Arg Phe Leu Lys Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu Lys Leu Gly Ile Lys Leu Pro Ile Gly Arg Asp Gly Ser Glu Pro Lys Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile 245 His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu 275 280 285 Lys Val Tyr Ala His Glu Ile Ala Glu Ala Trp Glu Ser Gly Glu Gly 295 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr 305 310 315 Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ile Gln Leu Ser Arg Leu 325 330 335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu 345 Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala 360 Pro Asn Lys Pro Ser Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn 390 Ile Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr 405 His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Glu Tyr 425 Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile 455 Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Ile Leu Leu Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly 490 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Leu Val Arg Lys Glu 520 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly 535 Leu Tyr Ala Thr Ile Pro Gly Gly Lys Ser Glu Glu Ile Lys Lys Ala Leu Glu Phe Val Asp Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys Lys Arg Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala Lys Val Leu Glu Thr Ile Leu Lys His Gly Asn Val Glu Glu Ala 625 635 Val Arg Ile Val Lys Glu Val Thr Gln Lys Leu Ala Lys Tyr Glu Ile 645 650

- Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Pro Pro Leu His 660 665 670
- Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala 675 680 685
- Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val 690 695 700
- Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu 705 710 715 720
- Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
- Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
 740 745 750
- Lys Glu Asp Leu Arg Tyr Gln Lys Thr Lys Gln Val Asp Leu Thr Ala 755 760 765
- Cys Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val 770 780
- Lys Phe Lys Tyr Lys Gly Glu 'Glu Lys Glu Val Asp Ile Ser Lys Ile
 785 790 795 800
- Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu 805 810 815
- Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro 820 825 830
- Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn 835 840 845
- <210> 34
- <211> 145
- <212> PRT
- <213> Artificial Sequence
- <220>
- <223> Description of Artificial Sequence:hybrid polymerase PhS3 from Figure 5
- <400> 34
- Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Ile Ile 1 5 10 15
- Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Val Glu Tyr Asp Arg
 20 25 30
- Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile 35 40 45
- Asp Glu Val Arg Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
 50 55 60
- Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
 65 70 75 80

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Glu Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile 95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr 1100

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115

Met Glu Gly Val Arg Tyr Arg Asn Pro Leu Ser Arg Arg Arg Arg Val Trp 145

<210> 35
<211> 844
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<212> PRT
<213> Artificial Sequence
<220>

<223> Description of Artificial Sequence:hybrid polymerase PhS4 from Figure 5

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg 20 25 30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile 35 40 45

Asp Glu Val Arg Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
50 55 60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65 70 75 80

Glu Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Ala Ile 85 90 95

Arg Glu Lys Val Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr 100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125

Met Glu Gly Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr 130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile 145 150 155 160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile 165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 180 185 190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr 200 Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Val Lys Arg Ala Glu 215 Lys Leu Gly Ile Lys Leu Pro Ile Gly Arg Asp Gly Ser Glu Pro Lys 230 Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile 250 His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr 265 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu 280 Lys Val Tyr Ala His Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Gly 295 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr 315 Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu 330 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu 345 Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala Pro Asn Lys Pro Ser Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser 375 Tyr Ala Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn 395 Ile Val Ser Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr 410 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asn Tyr 420 Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly Phe Ile Pro Ser Leu Leu Lys His Leu Leu Asp Glu Arg Gln Lys Ile 455 Lys Arg Lys Met Lys Glu Ser Gln Asp Pro Ile Glu Lys Lys Met Leu Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu 500 505 510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Arg Lys Glu 520 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Gly Leu 535 Tyr Ala Thr Ile Pro Gly Ala Lys Ser Glu Glu Ile Lys Lys Lys Ala 555 Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu Glu 570 Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys Lys Arg Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asn Val Glu Glu Ala Val 630 635 Arg Ile Val Lys Glu Val Thr Lys Lys Leu Ser Asn Tyr Glu Ile Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His Glu 665 Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala Ala 680 Lys Gly Val Lys Ile Arg Pro Gly Met Val Ile Gly Tyr Ile Val Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Val Gly Leu Thr Ala Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Ala Thr Val Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile Lys

810

Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu Gly

805

Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro Lys 820 825 830

Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn 835 840

<210> 36

<211> 845

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid polymerase PhS5 from Figure 5

<400> 36

Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile 1 5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
20 25 30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile 35 40 45

Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
50 60

Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65 70 75 80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile 85 90 95

Arg Asp Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr 100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125

Met Glu Gly Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr 130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile 145 150 155 160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile 165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 180 185 190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr 195 200 205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu 210 215 220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys 225 230 235 240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile 245 250 His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr 265 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu 280 Lys Val Tyr Ala Asp Glu Ile Ala Glu Ala Trp Glu Ser Gly Lys Asn 295 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu 330 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala 360 Pro Asn Lys Pro Asp Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr 405 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu Tyr 425 Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly 435 Phe Ile Pro Ser Leu Leu Lys His Leu Leu Asp Glu Arg Gln Glu Ile 455 Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Lys Met Leu 465 Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Leu Val Trp Lys Glu 520 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly 535 Leu Tyr Ala Thr Ile Pro Gly Gly Lys Pro Glu Glu Ile Lys Lys 550 555

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Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
                565
                                    570
Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys
                                585
Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
                            600
Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
                        615
Ala Arg Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
Val Lys Ile Val Lys Glu Val Thr Gln Lys Leu Ala Lys Tyr Glu Ile
                                    650
Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
                            680
Ala Arg Gly Val Lys Val Arg Pro Gly Met Val Ile Gly Tyr Ile Val
Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
                    710
                                        715
Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
               725
Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Val Gly Leu Thr Ser
Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
            820
                                825
Lys Glu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
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840

835

<210> 37

<211> 472

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid
 polymerase PhS6 from Figure 5

<400> 37

Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile 1 5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile 35 40 45

Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
50 55 60

Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65 70 75 80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile 85 90 95

Arg Asp Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr 100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125

Met Glu Gly Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr 130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile 145 150 155 160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile 165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 180 185 190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr 195 200 205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu 210 215 220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys 225 230 235 240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile 245 250 255

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr 260 265 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu 275 280 285

Lys Val Tyr Ala Asp Glu Ile Ala Glu Ala Trp Glu Ser Gly Lys Asn 290 295 300 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr 305 310 315 320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu 325 330 335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu 340 345 350

Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala 355 360 365

Pro Asn Lys Pro Asp Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser 370 380

Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn 385 390 395

Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr 405 410 415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu Tyr 420 425 430

Asp Val Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly 435 440 445

Phe Ile Pro Ser Leu Leu Lys Arg Leu Leu Glu Glu Arg Gln Lys Ile 450 455 460

Lys Arg Lys Met Lys Ala Thr Asn 465 470

<210> 38

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:region containing invariable sequence element from parental Pfu polymerase containing nucleotide binding motif

<400> 38

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
1 5 10 15

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu 20 25 30

Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu
35 40 45

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile 50 55 60

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<210> 39
<211> 60
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:region
      containing invariable sequence element from
      parental Deep Vent polymerase containing
      nucleotide binding motif
Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Arg Lys Glu
Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
                         55
<210> 40
<211> 60
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:region
      containing invariable sequence element from
      dedigmed hybrid polymerase containing nucleotide
     binding motif
<220>
<221> MOD_RES
<222> (1)..(60)
<223> Xaa = unknown amino acid
<400> 40
Asp Tyr Arg Gln Xaa Ala Ile Lys Xaa Leu Ala Asn Ser Xaa Tyr Gly
                                                          15
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
Ser Val Thr Ala Trp Gly Arg Xaa Tyr Ile Glu Xaa Val Xaa Lys Glu
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40

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
50 55 60

<210> 41

<211> 60 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:region containing invariable sequence elements from HyS1, Hyb2, Hyb3 and HyS4 hybrid polymerase containing nucleotide binding motif

<400> 41

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
1 5 10 15

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu 20 25 30

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu 35 40 45

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile 50 55 60

<210> 42

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:region
 containing invariable sequence element from PhS1
 hybrid polymerase containing nucleotide binding
 motif

<400> 42

Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly
1 5 10 15

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
20 25 30

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
35 40 45

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile 50 55 60

<210> 43

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:region
 containing invariable sequence element from PhS2
 hybrid polymerase containing nucleotide binding
 motif

<400> 43

Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
1 5 10 15

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu 20 25 30

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Leu Val Arg Lys Glu 35 40 45

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile 50 55 60

<210> 44

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:region containing invariable sequence element from PhS4 hybrid polymerase containing nucleotide binding motif

<400> 44

Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
1 5 10 15

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu 20 25 30

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Arg Lys Glu 35 40 45

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile 50 55 60

<210> 45

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:region containing invariable sequence element from PhS5 hybrid polymerase containing nucleotide binding motif

<400> 45

Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly

1 10 15

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu 20 25 30

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Leu Val Trp Lys Glu
35 40 45

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile 50 55 60

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<210> 46
<211> 60
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:region
      containing invariable sequence element from PhS7
      hybrid polymerase containing nucleotide binding
      motif
<400> 46
Asp Tyr Arg Gln Lys Ala Ile Lys Ile Leu Ala Asn Ser Phe Tyr Gly
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Phe Val Arg Lys Glu
Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile
                         55
<210> 47
<211> 6
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:6-His
      polyhistidine epitope tag, metal chelate affinity
      ligand
<400> 47
His His His His His
<210> 48
<211> 8
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:anti-DYKDDDDK
      epitope tag
<400> 48
Asp Tyr Lys Asp Asp Asp Lys
 1
                  5
<210> 49
<211> 45
<212> DNA
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<213> Artificial Sequence